

1.4 Predict Novel Associations

Now that we've got a trained *Mutual Interactors* model, we can use it to expand some node sets!

In particular, here we are going to use it to predict which proteins are associated with Tracheomalacia, a condition characterized by flaccidity of the supporting tracheal cartilage.

To do so, we specify the set of proteins associated with Tracheomalacia using GenBank IDs.

```
In [309]: # Specify a set of proteins by their GenBank IDs
# For example, we use the proteins associated with Tracheomalacia
# Swap out these GenBank IDs for another set of proteins!
tracheomalacia_proteins = ['COL2A1', 'HRAS', 'DCHS1', 'SNRPB', 'ORC4', 'LTBP4',
                           'FLNB', 'PRRX1', 'RAB3GAP2', 'FGFR2', 'TRIM2']
```

```
In [303]: # Show the visualization!
# Red nodes are the seed nodes fed to the model.
# Orange nodes are predicted nodes. Blue nodes are the interactors between them.
cy_vis
```

